

032301.159.seq.ST25.txt
SEQUENCE LISTING

<110> MOCKEL, Bettina

<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE cstA GENE

<130> 032301 WD 195

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 2718

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (200)..(2515)

<223>



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tggccgaact ttcctttttc tgcattgcatt tctgcacaca gtttctgccc gctgtttctg 180

cccgtgtttt ctacgcata gtg gct ttg aaa cga ccc gaa gag aaa aca gta 232

Met Ala Leu Lys Arg Pro Glu Glu Lys Thr Val
1 5 10

aag atc gtg acc ata aaa cag act gac aac atc aat gac gat gat ttg 280

Lys Ile Val Thr Ile Lys Gln Thr Asp Asn Ile Asn Asp Asp Asp Leu
15 20 25

gtg tac agc aac gct act gac ctt cca gta ggc gtg aag aag tcc cct 328

Val Tyr Ser Asn Ala Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro
30 35 40

aaa atg tca ccg acc gcc cgc gtt ggt ctc ctt gtc ttt ggg gtt atc 376

Lys Met Ser Pro Thr Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile
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gcg gcg gtg ggt tgg gga gca atc gct ttc tcc cgt ggc gaa aca atc 424

Ala Ala Val Gly Trp Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile
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aac tct gtg tgg ctg gtt ttg gcg gca gtt ggt tcc tat atc att gcg 472

Asn Ser Val Trp Leu Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala
80 85 90

ttt tct ttc tat gcc cga ctg att gaa tac aaa gtt gtt aag ccg aaa 520

Phe Ser Phe Tyr Ala Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys
95 100 105

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sub
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Val	Pro	Thr	Asp	Arg	Arg	Val	Leu	Phe	Gly	His	His	Phe	Ala	Ala	Ile	
125						130						135				
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Ala	Gly	Ala	Gly	Pro	Leu	Val	Gly	Pro	Val	Met	Ala	Ala	Gln	Met	Gly	
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Tyr	Leu	Pro	Gly	Thr	Leu	Trp	Ile	Ile	Leu	Gly	Val	Ile	Phe	Ala	Gly	
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cgc	tca	ctt	ggc	cag	atg	gtt	cgt	gat	gaa	atg	ggc	acg	gtc	ggg	gga	808
Arg	Ser	Leu	Gly	Gln	Met	Val	Arg	Asp	Glu	Met	Gly	Thr	Val	Gly	Gly	
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Val	Leu	Ala	Leu	Ile	Val	Val	Asn	Ala	Leu	Ala	Asp	Ser	Pro	Trp	Gly	
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tgg	ctg	ctg	ctt	gca	ccg	cgc	gat	tac	ctg	tct	acc	ttt	atg	aag	atc	1192
Trp	Leu	Leu	Leu	Ala	Pro	Arg	Asp	Tyr	Leu	Ser	Thr	Phe	Met	Lys	Ile	
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ggc	gtc	atc	ggg	ctg	ttg	gca	gtg	ggg	att	ttg	ttc	gca	cgt	cct	gag	1240
Gly	Val	Ile	Gly	Leu	Leu	Ala	Val	Gly	Ile	Leu	Phe	Ala	Arg	Pro	Glu	
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ggc gca ctg tct ggt ttc cac gca ctg att tct tca gga acc aca cca Gly Ala Leu Ser Gly Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro 380 385 390 395	1384
aag ctt gtg gag aag gaa tcc cag atg cgc atg ctc ggc tac ggc ggc Lys Leu Val Glu Lys Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly 400 405 410	1432
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att ctg gat cgt cac ctg tac ttc tcc atg aac gct ccg ctg gca ctg Ile Leu Asp Arg His Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu 430 435 440	1528
act ggt gga gat cca gca acc gca gct gag tgg gtt aac tcc att ggg Thr Gly Gly Asp Pro Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly 445 450 455	1576
ctg aca ggt gcg gat atc acc ccg gaa cag ctg tcg gaa gct gct gaa Leu Thr Gly Ala Asp Ile Thr Pro Glu Gln Leu Ser Glu Ala Ala Glu 460 465 470 475	1624
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cct tca tgg act gtc ggt aac tgg att tct acc gtg ttt gtg tgt gct Pro Ser Trp Thr Val Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala 560 565 570	1912
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tac aag tgg gcg tgg att cca gct gtt cct ttg gca tgg gat ctc att Tyr Lys Trp Ala Trp Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile 620 625 630 635	2104
gtc acg atg act gcg tca tgg cag aag att ttc cac tct gat ccg gct Val Thr Met Thr Ala Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala 640 645 650	2152
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tcc atc agg gct cgt gca gcc gga aca cct ttg gag acc act gaa gag Ser Ile Arg Ala Arg Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu 720 725 730	2392
cct gat act gaa tct gag ttc ttc gcc cca act gga ttc ctt gca tct Pro Asp Thr Glu Ser Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser 735 740 745	2440
tcc agg gat aag gaa gtc cag gcc atg tgg gac gag cgc tac cca ggc Ser Arg Asp Lys Glu Val Gln Ala Met Trp Asp Glu Arg Tyr Pro Gly 750 755 760	2488
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cacggcgatat tccaagtatg tgggtgcactt aaagcaccac catccggatg ctccgattcc	2655
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Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp
 50 55 60

Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu
 65 70 75 80

Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala
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Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr
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Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg
 115 120 125

Arg Val Leu Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro
 130 135 140

Leu Val Gly Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr
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Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr
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Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln
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Met Val Arg Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu
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Ala Thr Ile Ser Ile Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile

210

215

220

Val Val Asn Ala Leu Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr
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Met Thr Ile Pro Ile Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu
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Arg Pro Gly Arg Val Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu
 260 265 270

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Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile
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Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala
 305 310 315 320

Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu
 325 330 335

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Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser
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Leu Phe Pro Phe Leu Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly
 370 375 380

Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys
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Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser
 405 410 415

Phe Val Ala Met Met Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His
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Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro
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Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe
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Trp Tyr His Phe Ala Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr
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Val Asp Ala Gly Thr Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu
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Gly Asn Val Pro Gly Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val
545 550 555 560

Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile
565 570 575

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580 585 590

Pro Leu Phe Gly Ile Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala
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Leu Val Leu Val Val Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp
610 615 620

Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala
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Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala
645 650 655

Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe
660 665 670

Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr
675 680 685

032301.159.seq.ST25.txt

Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val
690 695 700

Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg
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Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser
725 730 735

Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu
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ggtatgacta gcccactct aaatgggtgta ggtatggtata aatcatctct caatgttact 180
tttccattgt taagaattaa caactctcgg tgatttgctg catacccagc tgtcaaagat 240
ccgatcatcg gcatacagaa acacccatct ggccgaactt tcctttttct gcatgcattt 300

032301.159.seq.ST25.txt

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Lys Arg Pro Glu Glu Lys Thr Val Lys Ile Val Thr Ile Lys Gln Thr
5 10 15

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Asp Asn Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala Thr Asp Leu
20 25 30 35

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Pro Val Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr Ala Arg Val
40 45 50

ggc ctg ctt gtc ttt ggg gtt atc gcg gcg gtg ggt tgg gga gca atc 549
Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp Gly Ala Ile
55 60 65

gct ttc tcc cgt ggc gaa aca atc aac tct gtg tgg ctg gtt ttg gcg 597
Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu Val Leu Ala
70 75 80

gca gtt ggt tcc tat atc att gcg ttt tct ttc tat gcc cga ctg att 645
Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala Arg Leu Ile
85 90 95

gaa tac aaa gtt gtt aag ccg aaa gat cag cga gca acc ccg gcg gaa 693
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Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg Arg Val Leu
120 125 130

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Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro Leu Val Gly
135 140 145

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Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr Leu Trp Ile
150 155 160

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Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr Leu Val Leu
165 170 175

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Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln Met Val Arg
180 185 190 195

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Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu Ala Thr Ile
200 205 210

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Ser	Arg	Thr	Gly	Gly	Ala	Pro	Thr	Leu	Ala	Phe	Gly	Met	Ser	Glu	Ile	
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Leu	Ser	Gly	Phe	Ile	Gly	Gly	Ala	Gly	Met	Lys	Ala	Phe	Trp	Tyr	His	
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Phe	Ala	Ile	Met	Phe	Glu	Ala	Leu	Phe	Ile	Leu	Thr	Thr	Val	Asp	Ala	
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ggg	act	cgt	gtg	gct	cgc	ttt	atg	atg	acc	gat	acc	ttg	ggc	aat	gtt	1989
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cca	ggg	ctg	cgc	cgt	ttc	aag	gat	cct	tca	tgg	act	gtc	ggg	aac	tgg	2037
Pro	Gly	Leu	Arg	Arg	Phe	Lys	Asp	Pro	Ser	Trp	Thr	Val	Gly	Asn	Trp	
		550					555					560				
att	tct	acc	gtg	ttt	gtg	tgt	gct	cta	tgg	ggg	gct	att	ttg	ctc	atg	2085
Ile	Ser	Thr	Val	Phe	Val	Cys	Ala	Leu	Trp	Gly	Ala	Ile	Leu	Leu	Met	
	565					570					575					
ggg	gtt	acc	gat	cca	ctg	ggc	ggc	atc	aac	gtg	ctt	ttc	cca	cta	ttc	2133
Gly	Val	Thr	Asp	Pro	Leu	Gly	Gly	Ile	Asn	Val	Leu	Phe	Pro	Leu	Phe	
580					585					590					595	
ggg	atc	gct	aac	cag	ctg	ctc	gcc	gct	att	gca	ctt	gct	ctc	gtg	ctg	2181
Gly	Ile	Ala	Asn	Gln	Leu	Leu	Ala	Ala	Ile	Ala	Leu	Ala	Leu	Val	Leu	
				600					605					610		
gtt	gtt	gtg	gtg	aag	aag	ggc	ctg	tac	aag	tgg	gcg	tgg	att	cca	gct	2229
Val	Val	Val	Val	Lys	Lys	Gly	Leu	Tyr	Lys	Trp	Ala	Trp	Ile	Pro	Ala	
			615					620					625			
gtt	cct	ttg	gca	tgg	gat	ctc	att	gtc	acg	atg	act	gcg	tca	tgg	cag	2277
Val	Pro	Leu	Ala	Trp	Asp	Leu	Ile	Val	Thr	Met	Thr	Ala	Ser	Trp	Gln	
		630					635					640				
aag	att	ttc	cac	tct	gat	ccg	gct	att	ggc	tac	tgg	gct	cag	aac	gcg	2325
Lys	Ile	Phe	His	Ser	Asp	Pro	Ala	Ile	Gly	Tyr	Trp	Ala	Gln	Asn	Ala	
	645					650					655					
aac	ttc	cgc	gat	gca	aag	tct	caa	ggc	ctt	acc	gaa	ttt	ggg	gcc	gct	2373
Asn	Phe	Arg	Asp	Ala	Lys	Ser	Gln	Gly	Leu	Thr	Glu	Phe	Gly	Ala	Ala	
660					665					670					675	
aaa	tct	cct	gag	gca	atc	gat	gcg	gtt	atc	cga	aac	acc	atg	att	cag	2421
Lys	Ser	Pro	Glu	Ala	Ile	Asp	Ala	Val	Ile	Arg	Asn	Thr	Met	Ile	Gln	
			680						685					690		

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ggc atc ttg tcc atc ctg ttc gcg gtg ctc gtc ctc gtt gtt gtc ggc 2469
Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val Val Val Gly
695 700 705

gca gcc att gcg gtg tgc atc aag tcc atc agg gct cgt gca gcc gga 2517
Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg Ala Ala Gly
710 715 720

aca cct ttg gag acc act gaa gag cct gat act gaa tct gag ttc ttc 2565
Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser Glu Phe Phe
725 730 735

gcc cca act gga ttc ctt gca tct tcc agg gat aag gaa gtc cag gcc 2613
Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu Val Gln Ala
740 745 750 755

atg tgg gac gag cgc tac cca ggc ggt gcg ccc gtg tct tct gga ggg 2661
Met Trp Asp Glu Arg Tyr Pro Gly Gly Ala Pro Val Ser Ser Gly Gly
760 765 770

cac taaaacatga tggctcttac tcatgcactg tggaaaatcc cgcgggcggt 2714
His

gtggtggtat ctactgagc tcatggggga cacggcgtat tccaagtatg tgggtgcactt 2774

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Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr
35 40 45

Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp
50 55 60

Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu
65 70 75 80

Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala

Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr
 100 105 110

Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg
 115 120 125

Arg Val Leu Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro
 130 135 140

Leu Val Gly Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr
 145 150 155 160

Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr
 165 170 175

Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln
 180 185 190

Met Val Arg Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu
 195 200 205

Ala Thr Ile Ser Ile Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile
 210 215 220

Val Val Asn Ala Leu Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr
 225 230 235 240

Met Thr Ile Pro Ile Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu
 245 250 255

Arg Pro Gly Arg Val Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu
 260 265 270

Leu Leu Ala Ile Val Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly
 275 280 285

Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile
 290 295 300

Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala
 305 310 315 320

032301.159.seq.ST25.txt

Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu
325 330 335

Leu Ala Val Gly Ile Leu Phe Ala Arg Pro Glu Val Gln Met Pro Ser
340 345 350

Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser
355 360 365

Leu Phe Pro Phe Leu Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly
370 375 380

Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys
385 390 395 400

Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser
405 410 415

Phe Val Ala Met Met Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His
420 425 430

Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro
435 440 445

Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp
450 455 460

Ile Thr Pro Glu Gln Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser
465 470 475 480

Thr Val Ile Ser Arg Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met
485 490 495

Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe
500 505 510

Trp Tyr His Phe Ala Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr
515 520 525

Val Asp Ala Gly Thr Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu
530 535 540

Gly Asn Val Pro Gly Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val
545 550 555 560

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Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile
565 570 575

Leu Leu Met Gly Val Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe
580 585 590

Pro Leu Phe Gly Ile Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala
595 600 605

Leu Val Leu Val Val Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp
610 615 620

Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala
625 630 635 640

Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala
645 650 655

Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe
660 665 670

Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr
675 680 685

Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val
690 695 700

Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg
705 710 715 720

Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser
725 730 735

Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu
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20